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The Pest and Pesticide Management Project
of the Consortium for International Crop Protection (CICP)

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IBSNAT, the International Benchmark Sites Network for Agrotechnology Transfer, is a group consisting of the contractor (the University of Hawaii) and several collaborators. Together they have created a prototype network of national, regional, and international agricultural research centers for the purpose of developing, validating, and using a scientific method for the effective transfer of agrotechnology among and within countries in the tropics and subtropics.

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PREFACE

Interest in developing coupled models (models of pests linked to crops) is steadily increasing. This interest comes from both disciplines, and is driven by a number of different factors. From the pest standpoint, the coupling can be viewed as providing a realistic representation of the host plant as a foundation or driving factor in a more detailed model of the pest population. From the crop standpoint, pests are stress factors for the crop grown and thus represent production constraints. In a single-species crop model, it is difficult to represent this stress accurately. Models of productions systems that include crop and pest provide more than the sum of their component parts. The coupling provides a method of understanding the host-parasite relationship at a fundamental level, and serves as a basis for defining yield-loss relationships that may be useful for predicting crop loss. Modeling a crop and its related pest organisms within the same space and time framework provides a challenge for the modeler and biologist, and also constitutes the next stage in producing integrated agricultural system models. We are fortunate that this workshop has allowed a group of researchers to meet and exchange their ideas and the techniques they have used in developing coupled pest-crop models.

Paul S. Teng

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Workshop on
Modeling Pest-Crop Interactions

January 7, 1990

Roy K. Nishimoto
Acting Director
Hawaii Institute of Tropical Agriculture and Human Resources

On behalf of the College of Tropical Agriculture and Human Resources, it is my pleasure this morning to welcome you to this workshop on modeling pest-crop interactions. Our dean, Ned Kefford, extends his sincere regrets in not being able to be here with you as he is fulfilling his role as Administrative Advisor for a Western Regional research project in New Mexico.

We are pleased to serve as co-sponsers to this workshop. I particularly commend the International Benchmark Sites Network for Agrotechnology Transfer (IBSNAT) Project as the driving force behind the workshop on modeling pest-crop interactions. I know that the IBSNAT Project has wanted to pursue this type of research activity for many years, and we are delighted that Paul Teng and Jonathan Yuen from the Department of Plant Pathology are now involved in this activity.

As you may know, Dr. Teng collaborated with the IBSNAT Project before he joined the University of Hawaii as Chairman and Professor of Plant Pathology. For example, while at the Department of Plant Pathology at the International Rice Research Institute, he wrote the article on "Pests and Pest-Loss Models" which appeared in the October 1988 issue of *Agrotechnology Transfer*. We are pleased that Dr. Teng is now with us and providing leadership in this area for the IBSNAT Project.

Although the IBSNAT Project really began in 1982, I consider its focus defined in 1974 with the Benchmark Soils Project. That project dealt with agroproduction technology and transfer by analogy. In other words, where soils are similarly classified, there should be similar crop response. The IBSNAT Project broadened the Benchmark Soils project from soils to sites, which includes soil and all other factors, such as environmental conditions, that influence agroproduction. IBSNAT also broadened the transference methodology from analogy to one that combines elements of transfer by analogy with systems analysis and simulation. IBSNAT has been developing a decision support system by combining soil, crop, weather, and farm management data bases with simulation models and expert systems. In September 1989, the IBSNAT Project reached a major milestone when they began distributing the software and User's Guide for the Decision Support System for Agrotechnology Transfer (DSSAT V 2.1) to user groups around the world. Gordon Tsuji from the IBSNAT Project will bring you up to date on that development later in the program.

You, as crop protection scientists, will recognize that the pest and disease components can have a major influence on crop production, and must be an integral part of any crop simulation model.

The modeling of pest-crop interactions is a very complex one as it involves many dimensions. We all know that crop response is dependent on many factors, such as plant nutrition or temperature which influences both growth and developmental processes, or light which affects the extent of growth that occurs as well as triggering developmental processes. At the same time, these factors could also influence the way in which pests and diseases may affect the crop. The choice of a crop cultivar could alter the yield and quality potential of a

given crop, as well as greatly alter its susceptibility to pests and diseases. When you add the complexity of pathotypes with various degrees of pathogenicity under various temperatures, humidity, and other climatic influences, one can quickly see the complexity of pest-crop modeling.

Thus, when we deal with an infinite number of combinations that could influence the manner in which pest-crop interactions can occur, I am impressed with those who pursue this research endeavor. An important goal of scientific inquiry is enhancing the predictability of events, and any advancement that we can make in this regard greatly increases our ability to manage crops more effectively.

When we can focus that thinking to that which has already occurred through the IBSNAT Project, I believe that you have an opportunity to make significant advances, and I thank you for participating in this workshop. I wish you the very best in your interactions over the next few days.

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Development of Generic Crop Models for Pest Coupling

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IBSNAT's Purpose and DSSAT

The major goals of the International Benchmark Sites Network for Agrotechnology Transfer (IBSNAT) Project is to develop improved capabilities for transferring agricultural production technology from sites of origin to new locations, and to provide a useful support system for decision making. To reach these goals, IBSNAT is developing a systems approach which uses crop simulation models adapted to evaluate the potential of various soil and crop management alternatives.

For this approach to be successful, crop models must first be validated by comparing model predictions with observations from field experiments. Experiments are needed for validation under different weather, genetic, and management conditions. After the experiment is conducted, the soil, weather, and management data are entered into computer files, the files are converted to a format required by crop model inputs, and the same experiment is simulated. Crop model predictions can then be compared with actual experimental observations, and any differences between observed and simulated results can be analyzed.

The IBSNAT Project has accepted responsibility for developing several major food crop models. Four models (maize, wheat, soybean, and peanut) have been adapted to IBSNAT standards and are available for validation by collaborators at their sites. Additional models for rice, dry bean, potato, barley, millet, sorghum, cassava, and aroid are in various stages of development and most are available for testing. The crop models require similar inputs of soil, weather, and management data, and all produce similar types of outputs of soil responses, crop growth, and yield data.

IBSNAT has developed an integrated computer system called the Decision Support System for Agrotechnology Transfer (DSSAT V.2.1). The DSSAT system consists of several components: 1) crop models; 2) soil and weather data; 3) collaborators' experimental data; and 4) application programs to enter and retrieve data, link the models with site and experimental data files, and analyze the observed and simulated data for specific objectives. We now wish to add a pest component to DSSAT.

Pest Linkages

Farmers have to make critical decisions about when to start applying a pesticide, how often to apply it, and when to stop. Predictive systems are badly needed for this purpose because of increasing economic pressures and environmental concerns. Crop models where properly validated can provide scientists with a) a reliable means to incorporate the crop as a component in pest models, b) a reliable means to estimate pest-free yield and pest infested yield under variable conditions, and c) a means to develop least loss strategies due to specific pests. Pest models also need to be validated and able to provide reliable information on pest populations and how environmental factors affect them. Pests often cause plant spatial patterns to be altered and the patchiness of the crop would also have to accounted for in the crop-pest model linkage (Hughes 1988). Most crop model and pest models can be run with the same set of weather data. There is little extra input information that is needed for running both. The critical need is to define linkage points between the two models. A linkage point is a known, quantifiable effect that a pest has on a crop. Pests can be classified according to their potential effects on a crop (i.e., the type of linkage points). A listing of linkage points follows (Boote et al. 1983; Teng 1988).

1. **Stand reduction:** in which plant number and biomass are removed from a system (e.g., damping-off fungi).

2. **Photosynthetic rate reduction:** in which remaining host tissues have a reduced rate of carbon uptake (e.g., certain virus pathogens).

3. **Leaf senescence acceleration:** in which senescence or abscission of leaves is affected by a known level of the pest population (e.g., some leaf spotting fungi).

4. **Shading:** in which photosynthetically active radiation is removed from plant parts which can utilize it (e.g., weeds).

5. **Assimilate removal:** in which soluble assimilate otherwise used for plant growth and development are used by pests for their own growth and development (e.g., leafhoppers).

6. **Tissue consumption:** in which plant tissue is physically removed from the system (e.g., defoliating insects).

7. **Turgor reduction:** in which there is interruption of the vascular system to affect xylem and phloem transport (e.g., wilt pathogens).

8. **Metabolic diversion:** in which metabolites to be used by one type of host tissue or host part are diverted to another (e.g., root lesion nematodes).

9. **Resource competition:** in which the pest competes for and utilizes resources before they enter the plant (e.g., weeds).

10. **Translocation disruption:** in which the translocation system is rendered totally dysfunctional (e.g., the neck blast syndrome in rice).

11. **Tissue disruption:** in which the pest causes cells to be disoriented and disrupt (e.g., root lesion nematode, rust pathogens).

The coupling of a pest model to a crop model starts with identifying which of the linkage points best describes the particular pest-crop combination. With some pests, it may be possible to explain most of the effect in terms of just one coupling point, as with defoliation by the Colorado potato beetle on potato, in which case the effect of the pest population over time may be modeled by incorporating a defoliation curve.

Successful linkages of pest models to the IBSNAT crop models require that the pest models be functional types requiring daily time steps. Pest models should be developed along similar levels of detail as the crop models so that the two will be fairly similar in the time required for the simulation. Most truly mechanistic models require too much information and computer time for IBSNAT purposes. Rational empiricisms have to be developed that simplify a mechanistic system to make the models functional.

The IBSNAT Project is committed to incorporating a few prototype pest models into a new version of DSSAT. These prototype models will provide examples of the level of detail needed for other pest models. We hope that several of the participants in this workshop can help provide these initial models. When they are properly validated, they can then become an important part of the DSSAT system and thus provide valuable decision making support.

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Genetic Coefficients for the IBSNAT Crop Models

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Crop cultivars differ one from another in a whole array of morphological and other characteristics. Some of these characteristics have been documented by cultivar testing authorities, and summarized in lists for distribution to both the scientific and farming communities. Other cultivar characteristics have been documented and summarized by computer modelers, who have used the list so produced as inputs to dynamic simulation models. In this context, the characteristics for one cultivar have been termed the "genetic coefficients" for that cultivar. They can be defined as: Coefficients that summarize the way in which a specific crop cultivar divides up its life cycle, responds to different aspects of its environment (e.g., day length, temperature, moisture stress, disease organism), or appears/changes morphologically.

The number of potential genetic coefficients is very large. However, the general aspects of adaptation to any given environment are determined by a few responses, and it is these that have been taken into account in the current IBSNAT models.

For maize there are five coefficients. Three relate to development and the progression through the life cycle, while two relate to growth aspects. The development coefficients summarize either, a) the minimum duration of some of the phases that a corn plant passes through during its life cycle or, b) the modifications to these durations brought about by photoperiod. Not all phases of development, which are delimited by specific developmental stages, have genetic coefficients, some being assumed constant across all genotypes. The phases that are considered relate to: a) the juvenile phase, b) the tassel initiation phase, and c) the linear grain filling phase. The duration of the tassel initiation phase is presumed to be affected by photoperiod to a degree that is genotype dependent, with the response for each genotype being assumed linear with respect to photoperiod at values greater than 12.5 hours. The maize development coefficients are complemented by two growth coefficients that relate to seed set and seed growth.

The development coefficients for soybean are like those for maize. They can be broken into two categories: the minimum phase durations, and the phase length modifiers. Like maize, soybean durations are not expressed in terms of chronological time, but unlike maize, "biological days" rather than "degree days" are used. The phase duration coefficients in the soybean model are complemented by two phase length modifiers; one deals with the response to photoperiod, while the other deals with the threshold photoperiod for response to be observed. Also, as for maize, the development coefficients are complemented by a number of growth coefficients, with both vegetative and reproductive growth being considered.

Wheat is simpler than soybean, with the array of coefficients being somewhat similar to those for maize. Unlike maize and soybean, however, the coefficients are not presented as such, but are reduced to scale values running from zero for those genotypes showing minimum expression of the trait in question, to some upper value for those genotypes showing maximum expression.

Genetic coefficients can be determined in a controlled environment setting indoors or outdoors. The use of special facilities may not be appropriate for some crops, and situations, however, and a third approach in which coefficients are estimated from field data sets in which dates of phenological events and yield components such as grain number and weight

have been measured, may well be the one that will become most widely applied. Software for this has been developed by IBSNAT.

The genetic coefficients used in the IBSNAT crop models are thus coefficients that characterize certain aspects of a cultivar's performance. Coefficients determined in one region should be similar to those determined in other, possibly contrasting, regions. Until this is proven, however, the models should not be used in conditions different to those in which the coefficients were determined. Further, the array of genetic coefficients currently used does not encompass all aspects that may be of significance in determining the performance of a specified cultivar in a given region. Factors that relate to physical stresses, diseases and perhaps also insects, will have to be taken into account before model outputs can be used directly for decision making at the farm level in some areas.

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A Generic Model for Phytomer Ontogeny and Vertical Placement in Competitive Weed-crop Communities

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Detailed system process modeling of crop communities is needed to search and test for simplified extension models. Once a new end use is encountered, the process of "distilling" the simple model from the complex must be repeated.

At Illinois we have been working on a detailed weed-crop competition model in an effort to explore weed growth under various cultural practices and to derive extension models. As with all pests, spatial problems in predicting pest population dynamics must be accounted for. Considering the variety of weed growth strategies, spatial problems associated with the "population" of phytomers (leaf, node, and internode parts) on an individual should also be addressed.

We are working on a generic plant morphology and phenology model, in a general quest to extend existing plant models to other species, whether horticultural, weedy, or part of the natural ecosystem. As part of this effort we have developed a model for positioning mainstream and branch nodes within the canopy and for the timing of phytomer ontogeny, including the physiological processes involved.

The rate of appearance of new mainstem leaves (dV/dt), compared to the rate of leaf primordia initiation, is most linear with temperature. The phyllochron $(dV/dt)^{-1}$, is therefore a convenient unit by which to scale other developmental rates. Along these lines, the classical logistic rate equation for individual leaf area expansion can be written:

$$dA/dt = (2\ln(A_f - A_i)/D_e)A(1 - A/A_f)dV/dt$$

where A_f is the final value of A, A_i is the value of A at leaf appearance, and D_e is the number of leaves that appear while this leaf is expanding. This equation was derived by replacing V for t in the logistic equation. Physiological constraints can be integrated into this equation as:

$$A_f = (1/age)\int_0^{age} A_f\,\alpha\,dt$$

where α depends on the physiological state of the plant. This equation is solved as $A_f = A_{fo}\exp(\beta)$, where A_{fo} is experimentally determined under standard reference conditions and β is defined by:

$$d\beta/dt = (\alpha - 1)/age.$$

The elongation of the associated internode (or petiole) generally occurs concurrently with leaf expansion, and thus can be described by:

$$DI/dt = (1/A)\,(dA/dt)I(1 + \lambda/f_Q)$$

where l is the length of the organ, λ is a parameter, and f_Q is the average daily fraction of full sun at the level in the canopy; f_Q can be interpreted as mapping the effects of irradiance directly, or serving as a proxy variable for light quality. The above equations describe the expansion of leaf area and internode elongation for individual mainstream phytomers. Branch leaf appearance can be described by:

$$dVB/dt = (dV/dt)\Gamma(fQ - b2)/(b1 - b2) \qquad f_Q < b_1$$
$$dVB/dt = 0 \qquad f_Q < b_2$$

where $\Gamma = dV_B/dV$, is the ratio of branch: mainstem leaf appearance rates (determined under standard reference conditions), and b_1 and b_2 are parameters; branch leaf appearance decreases with decreasing f_Q and may be inhibited altogether.

The above equations predict the dynamics of the vertical movement of leaf area based upon the phenology and physiological state of the plant. When rates for individual phytomers are integrated, the position of the phytomer within the canopy can be determined by accounting for the dimensions of all subtending phytomers. In order to implement this system of rate equations, a model of light absorption during interspecific competition must be used.

The ground area over which leaf area indices are calculated for an interspecific canopy composed of a single weed and the crop row, can be determined by considering the architectural dimensions of the weed. The "birds-eye-view" area of influence (AOI) of the weed is approximated by the row length contained in the circle determined using the horizontal length of the longest branch as the radius. The leaf area index (LAI) within this interspecific canopy is then:

$$LAI_W = \text{Leaf Area per Plant} / (AOI * DBR_C)$$
$$LAI_C = \text{Leaf Area per Plant} / DBP_C/DBR_C$$

where W denotes the weed, C denotes the crop, DBR is the distance between the rows, and DBP is the distance between the crop plants.

The absorption of light by this canopy is approximated as the absorption by a rectangular hedgerow based upon the height and width of the hedgerow and the (solar altitude) x (leaf angle-class) interactions. Once this absorption is calculated, the hypothetical relative covered ground area (RCG), of a continuous (non-hedgerow) canopy with the same LAI, necessary to absorb the same amount of light is calculated (Mutsaers 1980). This RCG is calculated separately for diffuse and direct irradiance, and used to modify the light attenuation equations in order to calculate the irradiance at any level within the canopy. The average photosynthetic rate within a layer is then calculated, taking into account the interaction of the non-linearity in the single leaf photosynthetic light response curve with the leaf angle-class distribution (Goudriaan 1988).

As the individual internodes are elongating within the canopy, each phytomer is assigned to a discrete layer for calculation of the leaf area index within that layer. To prevent some layers from being unpredictably empty (due to the arbitrary assignment of layer boundaries), the total leaf area in each layer is calculated as the top-down three-layer moving average. This technique results in a monotonically decreasing fQ as the phytomer ages.

With proper parameter selection, the model can mimic the behavior of weeds such as *Abutilon theophrasti*, that branch vigorously when grown in the open but not when grown within a soybean crop canopy, as well as mimic the behavior of weeds such as *Xanthium strumarium*, that branch vigorously even when grown within the soybean canopy.

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Physiologically-based Simulation of Weed Crop Competition

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Optimal pest management strategies use control measures only when pest population levels are high enough to potentially cause significant crop loss. Paramount in this concept is the development of the pest population/crop loss relationship. Based on this relationship, a threshold damage can be determined, below which control measures are not warranted.

A regression equation is often fitted to the relationship between pest populations and crop loss to apply experimental results to other years and locations. But regression equations are based on yield loss data in the years and locations where the experiments were conducted. The results are often not transferable to other locations or years. Secondly, a regression equation considers crop loss as dependent only on pest damage. Many experiments have shown that cultural factors such as row spacing and fertility, and environmental influences such as rainfall, may affect the amount of crop loss resulting from pest injury. Additional terms may be added to the equation to account for cultural or environmental factors, but regressions with correlated independent variables often result in large or illogical coefficient estimates (McGiffen et al. 1988). Further, regression equations do not accurately reflect the physiological mechanisms that result in observed yield loss.

Physiologically-based simulation models are based on the processes that underlie the plant's response to pest injury. As a result, they are more likely to be transferable to situations beyond the data originally used in validation. Simulation models allow experimentation with a wider range of interacting factors than would be practical experimentally. Simpler regression and physiologically-based models may be more practical for many management applications (Spitters 1990). We have developed a model that simulated velvetleaf and soybean growth and competition (VELVET). We present VELVET to illustrate concepts useful in developing simulations of the effect of pest injury on crop damage, and demonstrate how simulations can be used as a tool for managing pests and to guide future research.

In studying pest-crop ecology, it becomes apparent that a multispecies canopy is made up of a number of discrete layers. Velvetleaf attempts to shade out its competitors by overtopping the soybean canopy and concentrating leaf area above soybeans. Shade tolerant weeds such as eastern black nightshade survive under the soybean canopy, and take advantage of the increased light intensity during soybean leaf fall to rapidly increase biomass. Insects and pathogen damage is often stratified in the canopy in a species dependent manner. Simulating a uniform block of leaf area throughout the entire field is especially unrealistic when pests are present.

VELVET simulates continuous environmental parameters such as temperature and light intensity from standard daily weather data. At the top of the canopy, the photosynthetically active radiation is then portioned into diffuse and direct light. VELVET divides the canopy into a user determined number of discrete horizontal layers, and determines the amount of light absorbed by each layer, discriminating between diffuse and direct flux. The leaf area of each species in each layer is determined. Each species receives photosynthetically active radiation in proportion to its share of leaf area in that layer. The light not absorbed by the layer passes through to lower layers. The calculation of the amount of light entering the top of a layer, amount absorbed by each species, and amount passing through is repeated throughout the canopy. Individual leaf photosynthetic rates are calculated after adjusting for temperature,

water stress, and light intensity. The individual leaf photosynthetic rates are summed for all of a species' leaves. The daily canopy assimilation rate is calculated after subtracting maintenance respiration, and the plant converts assimilates into growth of plant organs.

VELVET estimates daily rates of change in soil moisture content by summing rainfall, deep percolation, soil surface evaporation, and transpiration. Water lost from the leaves of each species is removed from soil storage in proportion to the relative mass of roots present in any given soil layer. Thus, if velvetleaf has 70 grams of root mass in the 20-40 cm depth, while soybean plants have 30 grams of root tissue in the same soil volume, then velvetleaf roots can remove 70% of the plant available water. Potential transpiration is determined using Penman equations, and actual transpiration is calculated as potential times a function of soil moisture availability. The ratio of actual to potential transpiration is used to adjust canopy assimilation for plant water balance.

Varying model parameters has revealed aspects of velvetleaf competition that warrant further study. Much attention has focused on weeds with increased resistance to triazine herbicides, but which have reduced photosynthetic rates. Our results indicate that velvetleaf can tolerate substantial decreases in photosynthetic rate and remain competitive. However, simulated soybean and velvetleaf competition is very sensitive to soybean leaf expansion rate and plant height. These findings should be explored further as possible means for increasing crop competitiveness.

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Use of Radiation Data to Develop Crop Loss Models

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Plants may respond to the effects of plant diseases by changes in color (chlorosis and necrosis), changes in plant morphology (wilting and stunting), or by leaf abscission (Nutter 1990). Each of these factors will affect the quality and quantity of spectral reflectance from plant canopies. Therefore, remote sensing technology may offer an alternative means to monitor plant disease epidemics and to estimate damage prior to harvest.

Crop loss models are often used to quantify the relationship between biotic plant stress and yield (Nutter 1989). Area under the curve, critical point, and multiple point models are techniques that have been used to quantify the relationship between disease intensity and yield loss. Visual assessments of disease intensity are commonly used to monitor disease progress, however, visual assessments are often subjective, tedious, and labor intensive.

Waggoner and Berger (1987) have suggested that measuring healthy green leaf area or healthy green leaf area duration (1 - Y) would have a better relationship to yield than disease intensity measurements (Y), where Y is the proportion of diseased plant tissue present and (1 - Y) is the proportion of healthy leaf area remaining. Leaf area index (LAI) is the agronomic variable commonly used as the input variable in some plant growth and yield prediction models. However ground measurements of leaf area are tedious and costly to perform (Asrar et al. 1984).

Multispectral scanners have been used to record radiation in the visible and near infrared regions of the electromagnetic spectrum (0.3 - 1.4 mm). Scanners may be hand-held or mounted on trucks, aircraft, or satellites. Nutter (1989, 1990) has demonstrated that percent reflectance measurements (800nm) can be used as the independent variable in critical point yield loss models. However, the relationship between reflectance and disease intensity, and reflectance and healthy leaf area has not been elucidated. Nutter (1989) has hypothesized that the measurement of percent reflectance in specific narrow wavelength bands may provide an indirect measure of healthy green leaf area. The purpose of this study was to quantify the relationship between percent reflectance of sunlight (800nm) and healthy leaf area, and to test Waggoner and Berger's hypothesis that healthy leaf area (1 - Y) is a better predictor of yield than visual measurements of disease intensity.

Inputs for Modeling Crop Loss

Experiments were performed to obtain a range of early season differences in LAI, dry weight, and disease intensity by: a) planting different seeding rates of Florunner (susceptible to late leaf spot) and Southern Runner peanut (moderately resistant to late leafspot), and b) by differentially reducing the apparent infection rate of late leaf spot to obtain a range of late leaf spot disease intensity levels. This was accomplished by treating peanuts with various concentrations of Bravo 720F (chlorothalonil), where 1X concentration = 1.3 kg/ha a.i. (Nutter 1986).

Experimental Results

The use of different seeding rates as well as different a.i. fungicide concentrations resulted in a range of LAI, dry weight, and disease intensity values which could be used in conjunction with ordinary least-square regression analyses to quantify the relationships of these variables

with percent reflectance and pod yield. There was a strong linear relationship between percent reflectance and LAI for both Florunner and Southern Runner peanut, whereby LAI increased as percent reflectance increased. Reflectance explained 96 and 93% of the variation in LAI in Florunner and Southern Runner, respectively in 1988, and 1989. Percent reflectance measurements had a strong relationship with LAI and dry weight for data pooled over a season, which indicates that the relationships between reflectance versus LAI and reflectance versus dry weight are constant over a season. Also, the slopes relating reflectance to LAI ranged from 0.13 to 0.17 in both Florunner and Southern Runner and were not significantly different indicating that a standardized equation using reflectance measurements may be used to estimate LAI in runner-type peanuts.

Reflectance data explained more of the variation (r^2) in pod yield of Florunner and Southern Runner than LAI, dry weight, and disease severity of percent defoliation data. For both varieties, percent reflectance measurements, when used as the independent variable to predict pod yield, provided lower standard errors of the estimate compared to other critical point measurements. Reflectance measurements also had lower coefficients of variation than LAI, dry weight, and visual disease intensity measurements. In addition to having the best relationship to yield compared with other assessment methods, percent reflectance measurements could be obtained, processed, and analyzed 5 to 10 times faster than other methods.

Discussion

Three processes often occur simultaneously when peanuts are grown in the southeastern United States. The first process involves the production of peanut leaves (and stems) over time to build leaf area. The second process occurs when early and/or late leaf spot causes leaf spotting (necrosis) and defoliation. This process reduces the absolute amount of healthy green leaf area available for intercepting solar radiation which is required for the third process; the conversion of photosynthate into yield (peanut pods). An increase in peanut growth (LAI) occurring simultaneously with an increase in disease (increase in lesion number, lesion expansion, and defoliation) and increased pod demand for photosynthate, are three processes that can be integrated and measured by recording percent reflectance over time, since percent reflectance measures the absolute amount of green leaf area present in real time. Several researchers have suggested that measurements of LAI or LAI duration would have a better relationship to yield than disease intensity measurements (Asrar et al. 1984; Carver and Griffiths 1981; Johnson 1987; Waggoner and Berger 1987).

This may be because disease intensity measurements are usually proportional estimates, i.e., the amount of diseased tissue divided by the total plant tissue (=Y). Thus, the amount of healthy tissue remaining (1 - Y), is also a proportional estimate having a value between 0 and 1. In addition, the use of proportional estimates raises a serious question concerning the modeling of yield losses. Does a 0.50 (50%) reduction in LAI due to disease in a crop with a potential LAI of 4.0 have the same effect on yield or yield loss when Y = 0.50 in a crop with a potential LAI of 6.0? Absolute measurements of LAI available to contribute to yield should provide a better relationship to yield. Carver and Griffiths (1981) found that there was a very good relationship between the effects of powdery mildew infection on LAI and yield in barley. Our data suggests that reflectance measurements can provide accurate estimates of the absolute levels of LAI and therefore reflectance measurements often have a good relationship with yield. Johnson (1987) has also postulated that the measurements concerning the effects of disease on radiation interception (reduced LAI) and/or radiation use efficiency, would provide useful inputs for crop loss modeling.

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DISPAR: A Microcomputer Program to Calculate Foliar Disease-pest Parameters in Pest-crop Modeling

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With the advent of quantitative epidemiology, some of the older disease-pest parameters such as percent leaves or leaf area damaged, etc., are not sufficiently specific to explain certain phenomena. This has lead to the identification and definition of specific new parameters for use in disease-pest forecasting, prediction of yield loss, evaluation of resistance, comparison of chemical control measures, etc. (Berger 1980; Fry 1975; Kushalappa 1984, 1989; Kushalappa and Lagessee 1981; Kushalappa and Santos 1981; Seem 1987; Vanderplank 1963; Waggoner 1986; Waggoner and Berger 1987). Use of specific and appropriate parameters in pest-crop modeling enables better interpretation of results. With the help of DISPAR it is possible to calculate various disease and pest-damage parameters commonly employed in modeling pest-crop interactions and thus giving an opportunity for the researcher to use multiple parameters to explain certain phenomena.

The microcomputer program DISPAR, an acronym for Pest-Disease Parameters, was written in FORTRAN. The executable version of the program was developed using Microsoft FORTRAN compiler 3.3. To run, DISPAR requires an IBM or IBM compatible microcomputer with 640 k RAM, hard disk, or a 3.5" or high density drive, a DOS version 2.0 or higher, and an ASCII or IBM personal editor. The program is menu driven and easy to use.

The program was employed to reduce data and to calculate various disease parameters from marked and randomly selected plants for which the leaf (or fruit) position is known or approximated. The program also could be used to calculate similar parameters based on any other visible damage, due to pests, nutritional deficiency, etc. The data inputs are individual leaf area (estimated directly or an average leaf-area-per-leaf-position-per-plot or a standard leaf area is used) and disease severity quantified as proportion of leaf area diseased, or the number of lesions per leaf, or based on Horsfall-Barratt scores (Berger 1980; James 1971). When the disease is quantified as lesions data on average lesion area must be collected. The total number of sampling dates, plants per date, and leaves per plant or branch that can be included in one plot are maximums of 15, 15 and 30, respectively; the value of each variable can be changed as long as the product of the three remains 6750 or less. A data input template is provided to enter data in the order required by the program.

The disease parameters calculated were current, cumulative and intrinsic proportions of leaves or leaf area without and with disease, and area and proportion of area under the host growth and disease progress curves. The current are the sampling entities (leaves) attached to plant, the cumulative are totals since the beginning of measurement, and the intrinsic is the proportion of asymptote or maximum leaves formed. The cumulative and intrinsic categories were subdivided into formed, fell and removed. The formed and fell are the entities that appeared and have fallen since the beginning, respectively, whereas the removal is the sum of cumulative entities fell and those currently diseased. From the removal data the healthy host area can be derived (HHA = 1 - proportion of host area removed). In addition, the reduced data, the totals per plot and leaf position, can be used for the calculation of various other plant pest-disease parameters.

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Multispecies Simulations: Problems and Approaches

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The state-of-the-art in crop simulation models does not account for the biological diversity found in farmers' fields. Insects, weeds, and an array of beneficial and pathogenic microorganisms join crop species to create multispecies crop communities. In many regions of the tropics, intercropping—the production of more than one crop in the same field at the same time—is the norm. Intercrops can be complex, with a dozen or more managed cultivars in a field.

The complexity of multispecies crop communities is a motivation for crop modeling. It is only through simulation that interspecific interactions, as affected by the environment can be defined, and their effect on crop yield resolved. Decision support systems based on such simulations should provide an aid for crop management.

Assuming continued growth in the speed and data handling capabilities of computers, multispecies simulations will be limited principally by the design of their model. How such models are designed is problematical, as certain approaches will not be workable. Current multispecies models are often designed for specific species combinations, such as a particular insect pest or a particular crop. While quick progress can be made on special agronomic problems, there are too many meaningful species combinations to model with this approach. The problem mushrooms as the number of species increases: 16 species (a modest number to select from) create over 65,000 possible species combinations. It is clearly not practical for research programs to conceptualize, code, and validate separate models for each combination.

Generic models provide one avenue for simplifying multispecies simulations. The goal of generic models is to provide one model that works for a range of different species, each species having its own set of input parameters. Generic models can be relatively simple and expandable, performing multispecies simulations with relative ease. Problems can arise when generic models fail to account for significant species differences. And while a model can be written for a range of species, resources are often not available to measure the input parameters for each species and validate the model predictions.

Another approach to multispecies models is to make use of existing single-species models. These models are often well established, having a long history of experimentation to measure input parameters and validate predictions. The models tend to be written by scientists with special expertise in the growth and physiology of the species and there is often a commitment to support and develop the model.

Making use of single-species models for multispecies problems has a number of benefits, but simply combining disparate single-species models is unworkable. Redundancies, where the species models each try to perform the same task, must be resolved. New code must also be added for the interspecific interactions not considered in the original models.

Two techniques can help in the process of building multispecies models from existing single-species models: the use of a systems hierarchical structure for model organization and the use of object-oriented programming. Both these techniques have been used in the development of CropSys (Caldwell 1990; Caldwell and Hansen 1990) and AGSYSTEM (Caldwell 1990).

CropSys is a simulation model for maize/soybean cropping system. The model was built from CERES-Maize V.2.0 and SOYGRO V.5.41. Code for the single-crop models, written in

FORTRAN, was broken into small submodels and reorganized within a system hierarchical program structure. The structure places code and data for solar geometry in the WORLD submodel. Weather files are read in the LANDSCAPE submodel to accommodate the effects of terrain on data measured at off-site weather stations. Much of the critical code is in the ECOSYSTEM submodel: the energy balance, nutrient balances, and primary productivity. The primary productivity function carries out much of the growth calculations of the original single-species models. Calculation for competition occurs in code located in the COMMUNITY submodel. CropSys is designed to work with IBSNAT's Decision Support System for Agrotechnology Transfer (DSSAT), and runs on IBM-compatible microcomputers.

CropSys is currently restricted to maize and soybean. This limitation is principally the result of the FORTRAN language. To explore the possibility of more generalized multispecies simulations, object-oriented programming was used to develop AGSYSTEM. AGSYSTEM is able to dynamically allocate memory for each species in a community, permitting any number of species (within the basic limitations of the computer hardware and operating system) in a field. AGSYSTEM, like CropSys, is organized around a systems hierarchy. In the same way multiple species can be simulated within the community, other hierarchical levels can also contain multiple components: multiple fields in a farm, multiple farms on a landscape, and multiple landscapes in a simulation. AGSYSTEM was written in the ACTOR language and runs under Microsoft Windows on IBM-compatible microcomputers.

Both CropSys and AGSYSTEM provide a foundation for multispecies simulations. They create frameworks under which independently validated submodels can be linked with other submodels. An approach such as this is required if we want to simulate communities in which a range of different crops, weeds, insects, and microorganisms/pathogens could potentially by found.

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SPORE DISPERSAL OF *PYRICULARIA ORYZAE* IN RICE: A SIMULATION MODEL

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A model was developed to simulate the dispersal and deposition of spores of the rice blast fungus, *Pyricularia oryzae* within and above the rice canopy. In the model, DISBL, the numbers of conidiophores, spores of *P. oryzae* formed and discharged on and from blast lesions are calculated and spore concentration and the number of spores deposited on susceptible and non-susceptible leaves within and above the rice crop are simulated. The calculation is performed every hour of a day by using data of distribution of leaf blades and blast lesions as well as microclimate data in the rice crop. The "Gradient Transfer Theory" of McCartney and Fitt (1985) was used in the model and the dispersal and deposition of *P. oryzae* spores determined by the modified equation by Legg and Powell (1979) and Inoue's equation reported by Suzuki (1969). The hourly variations of calculated concentrations of *P. oryzae* spores and vertical profiles of the spore concentrations in and above the rice crop were similar to the results reported by Kuribayashi and Ichikawa (1952), Suzuki (1969), and Ou et al. (1974). The calculated numbers of *P. oryzae* spores on horizontal slide glasses agreed with the measured ones. The simulation results using the model suggested that wind speed and leaf area index (LAI) of the rice crop affected the concentration and number of *P. oryzae* spores deposited within the rice canopy.

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Septoria nodorum In Wheat-A Coupled Simulation Model

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The purpose of this paper is to present a description of a crop-pest interaction model which simulates a *Septoria nodorum* epidemic in winter wheat. The model is not yet validated and at present serves as a framework for storing knowledge and identifying areas that require more information. The future objective is to use the model as one of the tools for forecasting *S. nodorum* epidemics.

Since the relationship between disease loss and disease severity is seldom simple, and since different environments as well as growth stages affect the magnitude of loss, a pure disease model is not satisfactory. To fill the purpose of the model, the host plant has to be considered as well. In most cases where the host plant is included in disease models it serves mainly as a substrate for the pathogen (Teng et al. 1977; Aust et al. 1983; Berger and Jones 1985). However, for studies where disease damage to the crop is included, the crop has to be described in more detail.

The model presented here consists of a crop module and a disease module that are linked together. It operates with a daily timestep and is driven by temperature, day length, solar radiation, evaporation, rainfall and number of hours when the difference between air temperature for a particular hour and dewpoint temperature is <1°C. The latter is used for calculation of leaf wetness duration. The model is written in Turbo Pascal and can be run on an IBM or IBM-compatible personal computer.

Wheat Growth

The wheat module is a modified version of a model based on phasic development. To adapt it for an epidemic caused by a foliage pathogen such as *S. nodorum* the leaf canopy was represented as individual leaf levels (representing the main stem leaves plus tiller leaves produced at the same time). For each of 10 levels plus the ear initiation, area and senescence was simulated. This was necessary to account for the variation of the pathogen's growth rate, which in turn depends on leaf age, and to know where the pathogen was present and to where it was dispersed. Plant weight increases by calculated net assimilate production which is translocated and partitioned within the plant.

Septoria

A disease module was added to the above wheat module in order to model the *S. nodorum* epidemic. Its main components are:

- the life cycle of the fungus
- parts dealing with lesion growth and vertical inoculum dispersal
- weather and host plant interactions.

In its life cycle the fungus goes through a number of development stages which include delays, i.e., latency period etc. These delays are simulated with Boxcar trains (Goudriaan and van Roermund 1989) and are, in this model, driven by lesion growth rate which is a function of temperature. The Multiple Infection Transformation (Gregory 1948) and its inverse is repeatedly used between the Boxcar trains to adjust the number of growing lesions to the leaf area available for lesion expansion.

The occurrence of spore extrusion and dispersal, as well as new infections that take place,

is linked to criteria of rainfall and leaf wetness duration. Disease development is simulated on each of 10 individual leaf levels plus the ear, and spores are dispersed between different leaf layers according to an exponential function.

Interaction

The model can be run with a range of weather types and initial disease conditions. At present, the effects of disease on the host plant and yield are twofold: the absolute reduction of photosynthesizing leaf area, and the decrease in the photosynthetic efficiency of remaining living tissue. The wheat module sends information on assimilating and senescent leaf area of individual leaf levels and their changes over time, to the disease module, and the disease module returns information on diseased leaf area in different development stages of the pathogen's life cycle to the wheat module. The structure of the model enables any other effects to be included in the future.

A coupled crop and disease model has several uses apart from prediction of disease levels. It is a means of integrating knowledge and identifying new research areas. Different interactions between disease, host, and environment, such as the dynamics of economic thresholds, can be studied. Since the model predicts grain yield, it can improve the understanding and estimation of yield loss. Finally, coupled models can serve as tools for work on disease management and risk analysis. By coupling disease, crop and environment into one model, we have a means of taking a more holistic approach to the concept of disease and crop interaction, and a way to gain more insights into how the system works.

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IMPACT OF PESTS ON CROPS: SPATIAL ISSUES

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IBSNAT crop models "assume uniform row spacing, plant count and seed depth. If uniformity is not maintained, then simulation results may not compare well with actual experimental results" (IBSNAT 1988). However, it is well known that pest attack on crops is usually patchy and results in irregular plant losses (Jones et al. 1955). What is the effect of such pest inflicted patchiness and how can it be incorporated into crop loss assessment models?

Two types of field experiment can help characterize the effect of patchy pest attack on crop yields. In one, a range of plant spatial patterns is incorporated in the experimental design. For example, Thomson (1956) showed that as the variance of the frequency distribution of in-row spacing increased, at constant plant population density, yield of sugar beet crop decreased. Generally, this effect tends to be greater at smaller densities rather than at larger densities. Such experiments can be regarded as field simulations of patchy pest attacks. Another type of experiment which may be of interest is one in which the crop (perhaps inadvertently) actually suffers a pest attack. Hughes et al. (1989) characterized the frequency distribution of in-row spacing from such a crop, and showed that yield losses with decreasing plant population, density, and a patchy spatial pattern of plants, were more severe than with decreases in density which did not involve disruption of a regular spatial pattern.

To place the effect of patchiness on the relationship between crop yield (Y) and plant population density (D) in a more general context we can start by writing:

$$\underline{Y} = \underline{f}(\underline{D}) \qquad [1]$$

where $\underline{f}(D)$ is often a nonlinear (concave) function of the form $\underline{f}(\underline{D}) = \underline{D}/(\underline{a} + \underline{b}\underline{D})$ in which $\underline{a}$ and $\underline{b}$ are parameters (Wiley and Heath 1969). If the plants are distributed more or less uniformly, we can estimate $\underline{Y}$ by first estimating $\underline{D}$ and then substituting this value into equation [1] to calculate $\underline{f}(\underline{D})$. However, if, as the result of a pest attack, the plants are actually non-uniformly distributed, the characteristics of $\underline{f}(\underline{D})$ cause this procedure to lead to an overestimate of yield. We should instead estimate $\underline{Y}$ by calculating:

$$\bar{\underline{f}}(\underline{D}) = \Sigma_i \underline{f}(\underline{D}_i)\Pr(\underline{D}_i) \qquad [2]$$

The question now is how to use this result to quantify the effects of spatial heterogeneity in crop loss assessment models without making excessive demands for input data.

If a spatially homogeneous $\underline{f}(\underline{D})$ is known, the effect of spatial heterogeneity can be simulated by substituting an explicit statistical distribution for $\Pr(\underline{D}_i)$ in equation [2]. In one such example, Hughes (1988) used the beta distribution, varying the parameters so as to obtain estimates of crop yield at a range of mean plant population densities and three different levels of aggregation. The results of this simulation were consistent with the suggestion that compensatory growth by a crop after a pest attack is reduced as the pattern of crop injury becomes increasingly aggregated, so providing a quantitative basis for the conceptual model envisaged by Jones et al. (1955).

Ferrandino (1989) presented an approximate method for the resolution of equation [2]

based on a Taylor-series expansion of $f(D_i)$ about $f(\bar{D})$:

$$f(D) = f(\bar{D}) + f''(\bar{D}) \cdot (s_D^2/2!) \qquad [3]$$

Thus $\bar{f}(D)$ is equal to $f(\bar{D})$ plus a correction factor which has the sign of $f''(\bar{D})$ (negative for a concave $f(D)$) and which increases in absolute value with the variance of D and the degree of non-linearity of the function. This method uses the data directly and does not depend on any fitted distribution to describe $Pr(D_i)$. Ferrandino (1989) demonstrated that the results were easily calculated and reasonably accurate.

A rather different type of spatially heterogeneous crop loss assessment model has recently been outlined by Hughes et al. (1989). This involves expressing the rate of yield loss per unit pest injury as a function of an index of aggregation, which in turn is expressed as a function of the mean level of pest injury. The simplest case is:

$$dI/dq = cI \qquad [4]$$

in which I is yield loss, q is mean level of pest injury, c is a proportionality constant and I is an index of spatial pattern which increases with increasing aggregation. If we can write $I = f(q)$, equation [4] may be integrated to give a loss assessment model of the form $I = f(q)$, which accounts implicitly for patchiness. Hughes (1990) has shown that when pest injury is expressed on an incidence scale and I is the ratio of observed to expected binomial variance, I can be written in terms of the incomplete beta-function. The resulting loss assessment model may be linear or sigmoid, depending on the value of a parameter which varies with the spatial pattern of plant injury.

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Pest Effects on Crop Growth and Yield

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The development of modern integrated pest management systems requires that the effects of pests and diseases on crops be quantified and predicted. This can be done by either using empirical damage functions, or by coupling pest effects dynamically with crop simulators.

Empirical damage functions quantify the "overall-effect" of pests or diseases on crops. They are most often based on regression approaches and therefore have limited applicability. They relate, sometimes in combination with crop variables, temporal features and the magnitude of disease- or pest progress curves to yield losses. We can roughly distinguish between single predictor models: single critical point, and area-under disease- progress-curve models, and multiple predictor models: multiple critical point, and response surface models. Empirical damage functions are discussed in detail by Madden (1983), Teng (1985, 1987, 1988), Waggoner and Berger (1987) and Walker (1987).

The use of crop simulators represents a mechanistic, physiologically based approach to predict pest effects on crops. It can thus provide insights into the mechanisms of growth and yield reduction and has potential applicability across years and locations (Boote et al. 1983; Rouse 1988; Teng 1988). This approach requires that the pest population level be quantified at any given time and linked to a crop simulator. But before simulating pest effects by means of crop models, "coupling points" have to be identified, i.e., the processes and pathways, where these effects specifically take place. Charles-Edwards (1982) pointed out that pests can principally affect the physiological determinants of crop growth: amount of intercepted light, light use efficiency, partitioning, rate of dry matter loss, and duration of plant production. According to Boote et al. (1983), diseases and pests can generally be classified based on the type of damage they incur on carbon flow and/or growth processes of plants, such as: stand reduction, photosynthetic rate reduction, leaf senescence acceleration, light stealing, assimilate sapping, tissue consumption, and turgor reduction. Based on these specific damage effects, the corresponding physiological pest-crop coupling points can be defined. Other coupling points such as respiration acceleration, transpiration enhancement, and leaf appearance reduction were identified by Rouse (1988) and Rabbinge and Bastiaans (1989). And, finally, Johnson (1987) has noted that there are only two major ways, in which pests can affect growth processes and that is: by altering the radiation interception, and by altering the radiation use efficiency.

One of the first coupled pest-crop model to be reported is that developed by Gutierrez et al. (1976). These workers also gave an example of consistent work by coupling different pests to the same cotton crop model (Gutierrez et al. 1975, 1977, 1983). Other examples of such consistent work are provided by Johnson (1988), Johnson et al. (1987), and Johnson and Teng (1989) for potato; and for wheat by Rabbinge and Vereyken (1980), Rabbinge and Rijsdijk (1981), Rabbinge and Bastiaans (1989), Roermund et al. (1986), and Rossing et al. (1989). Adams (1987) coupled a detailed, physiologically-based powdery mildew model to a sugar beet crop model, and the complex effects of aphids on wheat were modeled by Rabbinge and Vereyken (1980).

An example of coupling two pests to the same crop model at the same time is provided by Alocilja (1989), who coupled a leaf blast and a leaf folder model to the CERES-Rice model. The same crop model was used by Torres (1989) to simulate the effects of rice leaf blast. In

his example, the yield loss caused by panicle blast was predicted by means of an empirical damage function. In most of the above mentioned cases, only one, rarely two or more coupling points were used. Most frequently, the coupling points used were tissue consumption, followed by senescence acceleration, turgor reduction, and assimilate sapping.

Coupling pest effects to crop simulators can be useful for studying various aspects of pest-crop interactions. For example, Johnson and Teng (1989) coupled a disease progress model for early blight to a model for potato growth in order to examine the relative importance of different epidemiological parameters, and how changes in certain features of the epidemic development would affect the crop. Their results showed that leaf area index and final tuber yield reacted sensitively to the time of the epidemic onset and the infection rate respectively. Boote et al. (1983) who coupled a *Cercospora* leaf spot model to a peanut crop model, demonstrated that the light use efficiency decreased, as the disease level increased. Moreover, they could show how specific pest effects, such as senescence acceleration, self shading, and toxicity contributed to the total effect on photosynthesis. Similarly, Rabbinge and Vereyken (1980) traced back the total effect of aphids on wheat to more specific effects, that together explained the variation in dry matter production better than each one singly.

Clearly, coupled pest-crop models can be powerful research tools for identifying and studying pest effects on crops, as well as for simulating real time conditions. They can thus serve as advisory tools for better decision making. Even though recent progress on this matter has been considerable, there is still a lack of quantitative information regarding pest effects on different crop physiological processes, the proportionality of these effects, the interactions among several pests, the combined effects of these interactions, as well as regarding the effects of control measures, and the factors affecting crop resistance. Further needs also involve finding a common language among researchers regarding the physiological base for coupling, validating coupled models across years and locations, and defining the minimum data sets required to run coupled models.

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GHLSIM:
Sahelian Grasshopper/Crop Loss Simulation

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Grasshoppers and locusts periodically cause dramatic losses to crops and rangeland in the African sub-Saharan region known as the Sahel. The GHLSIM modeling system was created, under contract with the U.S. AID Africa Bureau, to provide decision makers a means of estimating feeding injury and economic losses by *Oedaleus senegalensis* (Krauss) in millet and sorghum grown in the Sahel (Coop et al. 1989).

GHLSIM consists of separate submodels for pest population dynamics, crop injury simulation, economic analysis, and aggregation of results from multiple sites. The modeling system also includes a pull-down menu user interface, data base entry screens for field site, insecticide, and crop data, and screens for entry of runtime and behavioral analysis options. Outputs include dates of major crop stages, predicted yield losses, treatment benefits, and benefit/cost ratios. Grasshopper dynamics are simulated by an expansion of the PRIFAS OSE biomodel (Launois and Launois-Luong 1985), and are initialized using density estimates from field surveys. Spatial resolution is site-specific as determined from field surveys and nearest weather station data. Yields and planting dates may either be input into data bases or estimated by a soil water-balance model (FAO 1986). Benefits of treatment tactics are estimated by simulating both a treated and a non-treated population and comparing resulting yield reductions. Second year benefits of treatment are estimated by breakeven analysis of potential damage from final eggpod densities of treated and non-treated grasshoppers.

Crop loss in GHLSIM v.1.0 involves accumulating crop injury units according to grasshopper stage-specific densities, dry matter consumption rates, crop preference factors, and crop growth stage-specific susceptibility factors. GHLSIM was used to analyze the 1987 late-season (phase II) grasshopper control operation at 14 sites in Chad (Coop et al. 1989). Yield increases from grasshopper treatment ranged from 0 to 323% ($\bar{x}$ = 47%), with densities ranging from 15 to 75/m^2 ($\bar{x}$ = 32/m^2). Favorable benefit/cost ratios ($\bar{x}$ = 4.2) were estimated, while treatment dates were estimated to have been ca. 5 days later than optimal.

Although the injury unit approach is adequate for estimating direct losses to the spike, it cannot easily handle the dynamics of earlier crop stage defoliation. A crop growth model was selected for use in GHLSIM V.2.0 to more realistically simulate early crop injury and subsequent regrowth under a variety of environmental stresses such as drought. CERES-Millet V.1.99 (IFDC 1989), like other CERES models, is intended to simulate major crop growth mechanisms anywhere in the world, given crop and soil coefficients and weather data.

We are modifying CERES-Millet for use with GHLSIM to allow direct coupling of grasshoppers to the crop. Other changes are being made to allow CERES-Millet to run in a batch environment, to use a weather data preprocessor to convert from the available 10 day (dekad) average data into daily data as required by the CERES models. Simulating grasshopper impact to mainstem and tiller leaves during leaf growth stages involves daily removal of leaf area, leaf mass, and stored nitrogen in proportion to the density, amount consumed, and feeding preference by each grasshopper stage. In preliminary defoliation tests, and from studies with CERES-Maize (Piper and Weiss 1990), it appears that recalibration/reworking of carbohydrate partitioning functions and reduction of kernel number in addition to kernel weight, will be needed to accurately simulate defoliator impact. Impact to the spike should include a spoilage factor and will be treated as a direct reduction in kernel weight and

number. Changes to allow efficient batch processing include a restructuring of input/output routines with switchable menus for experiment and treatment selection, stop and restart routines for allowing dynamic optimization, and inclusion of subfields for studies involving spatial heterogeneity.

The dekad to daily weather converter algorithm reads the weather files used by the OSE biomodel and outputs CERES-format weather data. The algorithm is based on temperature and radiation difference statistics for dry days and rain days and average size of rain events, which are generated by a separate utility program using daily historical weather data. Number of rain events during a dekad is determined by the historic size of rain events for that dekad. Rain events are timed uniformly over the dekad. The size of each event is the mean for the period. Since temperature and radiation tend to be lower on rain days than dry days, the historical temperature and radiation differentials are used to disaggregate the dekad means into rain and non-rain day means. This algorithm was calibrated and tested using data from Jodhpur, India. The generated data showed a bias to overpredict yields compared to the original data set. Improvements will be tested to decrease this bias. Although the incorporation of CERES-Millet into GHLSIM is not yet complete, we expect significant improvements in model predictive accuracy and flexibility.

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Assessing Potential Epidemics of Soybean Rust with Synthetical Approach

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Soybean rust, caused by *Phakopsora pachyrhizi*, causes significant yield losses in eastern hemisphere countries. The disease does not occur in the United States but has been considered a potential threat to U.S. agriculture. To assess the potential impact of this disease on U.S. soybean production, data and information have been collected through cooperation during the last decade between USDA Foreign Disease-Weed Science Research Unit (FDWSRU) and the Asian Vegetable Research and Development Center (AVRDC) in Taiwan. Due to the difficult nature of foreign disease study, these data were collected and analyzed by different people in different periods with inconsistent objectives. Therefore, previous threat analysis was quantitative in so much as it was based on only some disease components rather than the total system. Our aim was to produce a disease simulation model by integrating available information and reanalyzing the data to provide the information necessary for the model.

As part of the potential impact analysis conducted at FDWSRU, a soybean rust simulation model, SOYRUST, was developed to incorporate geographical information in the assessment. The simulation model is programmed with FORTRAN and runs both on an IBM mainframe or personal computer. It consists of a simple soybean leaf growth model (Yang et al. unpublished), three disease component models, and statistic and graphic subroutines.

Plant growth models used to calculate the growth of leaf area ($\underline{A}$) of a soybean population were: $\underline{A} = -353.57 + 34.01\underline{t}$, $\underline{r}^2 = 0.89$ ($\underline{P} = 0.0001$) for cultivar TK 5; and $\underline{A} = -332.68 + 20.1\underline{t} + 0.71t^2 - 0.005t^3$, $R^2 = 0.92$ ($\underline{P} = 0.0001$) for G 8587. The models were developed based on extensive data from sequential planting experiments consisting of 13 different planting times throughout the year in Taiwan. The $\underline{t}$ is the sum of physiological days for plants ($\underline{D}i$) calculated from daily average temperature ($\underline{T}_i$) using equation as:

$$D_i = (\underline{T}_{opt} - \underline{T}_i)/(\underline{T}_{opt} - \underline{T}_{min}) \text{ if } \underline{T}_i < \underline{T}_{opt} \text{ or } \underline{D}_i = (\underline{T}_i - \underline{T}_{opt})/\underline{T}_{max} - \underline{T}_{opt}) \text{ if } \underline{T}_i > \underline{T}_{opt}.$$

Leaf area of a plot was calculated after multiplying A by the number of plants/plot. The basic simulation unit is site of infection, equal to maximum size of a lesion. The number of increased sites per day is calculated by dividing increased leaf area (cm^2) by the size of a disease lesion.

Equations describing environmental effects on disease components were developed by reanalyzing published data (Marchetti et al. 1976). The infection rate (R) was successfully predicted using dew period ($\underline{D}$) and temperature ($\underline{T}$) as independent variables. The model is:

$$\underline{R} = 0.293 - 0.039\underline{D} - 0.115\underline{T} + 0.0111(\underline{DT}),\ R^2 = 0.88,\ \underline{P} < 0.0001.$$

Two thresholds for infection were established as $\underline{D} > 4$ hr and $\underline{T} < 27$ °C. The time required to complete the latent period was described with an exponential model using accumulative physiological days for the pathogen ($\underline{t}$) as an independent variable. The model was developed by reanalyzing data from Yeh et al. (1982) and is written as $\underline{R} = 1\text{-exp}(-0.302\ (\underline{t} - 6.35))$, $\underline{P} < 0.0001$. The progress rate of a disease lesion from infectious to senescent was

developed using the same method and described as:

$$\underline{R} = 1 - \exp(-0.306(\underline{t} - 18.51)),\ \underline{P} < 0.0001.$$

The simulation model was validated in two steps. First, it was extensively validated and calibrated with data from two sequential planting experiments consisting of 72 planting dates at weekly intervals during 1980 and 1981 in Taiwan. Two susceptible cultivars TK 5 and G 8587 were used. Epidemic development of each planting was rated 8-16 times and each epidemic had a different environmental window because of differences in planting date. The model was driven using weather data from fields, and the predicted severities were plotted and regressed against the observed data. Two parameters affecting disease development, lesion size, and maximum day temperature, were calibrated based on previous data (Melching et al. 1979). The regression coefficient ($\underline{B}_0$ and $\underline{B}_1$) and coefficient of determination (r^2) were plotted against their expected values by year x cultivar combination to examine the variation pattern. The expected values of $\underline{B}_0$, $\underline{B}_1$, and r^2 were 0, 1, and 1, respectively.

The model accurately reflects the effect of environment on disease development as shown by the results that predicted epidemic curves had similar trends to those observed, which varied from season to season. The epidemic onset stage varied from 25-60 days for TK 5 and 50-80 days for G 8587 after planting. The epidemic reached the maximum 75-95 and 100-120 days after planting for TK 5 and G 8587, respectively. The accuracy of prediction of disease onset stage was demonstrated by values of $\underline{B}_0$ which were close to zero with a deviation of less than 10% during the planting seasons. The consistency of predicted disease severities compared to the observed in regular planting seasons was shown by the values of $\underline{r}^2$ and $\underline{B}_1$ which were greater than 0.85 and 0.9, respectively. For epidemics during 1980 presummer (Day 80-150 for TK 5 and 80-180 for G 8587) and winter planting (Day 0-30 and Day 300-365), results of prediction were not as good as those from normal planting seasons, shown by the lower $\underline{r}^2$ and $\underline{B}_1$. The deviation between expected and calculated coefficients was less in TK 5 than in G 8587 during these periods. For the results of 1981, the deviation of presummer planting was less than those of 1980. In general, the results with TK 5 were better than those with G 8587.

The second step of validation involved running the model with data not used in model development. The data were from resistance screening experiments conducted during three regular planting seasons during 1979 and 1980, using the same varieties. With these data, the model successfully predicted disease development. Times of onset varied from 25 days (autumn, 1980) to 50 days (spring, 1979) after planting; the onset time was accurately predicted by the simulation model. The predicted disease curves fit the observed ones closely although the epidemic period of three growing seasons varied from 65 days (autumn, 1980) to 95 days (spring 1979) in TK 5 and 80 to 112 days in G 8587. However, the simulation model often underestimated the disease development after disease severity was greater than 90%. For G 8587, results of the summer planting had greater deviation between calculated and expected coefficients than those of TK 5. Disease severity of G 8587 was low in 1979 due to the existing resistance of the cultivar to the rust pathogen. The simulated disease severities fit the observed reasonably well after multiplying a correction factor of 0.8 to the infection rate.

There are several sources of variation which the model does not explain. Variation may be from the initial inoculum which was assumed to be constant for all the planting times. The soybean plant growth model used in the simulation model was merely empirical, which does not include the plant photoperiod reaction. Photoperiod reaction of plants may be a source of variation. However, these variations may become measurable by coupling the disease model with a soybean model which simulates plant growth at the processing level, such as SOYGRO. For the purpose of assessing potential rust severity in the United States, this simulation model

may be sufficient to reflect the effect of geographic difference on disease development. If the seasonal environmental differences can be related to geographic differences which influence disease epidemics, it appears the model may be able to take into account the geographic difference and, therefore, have the potential applicability for impact assessment.

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Coupling a Growth Model to a Peanut Rust Model

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Introduction

Peanut rust and leaf spot are two major foliar diseases of peanut in western Africa. A first attempt was made to build a simulation model for peanut rust which is a newcomer in this part of the world. This work was undertaken as part of a cooperative project between ORSTOM (Office de la Recherche Scientifique et Technique Outre-Mer), and the Wageningen Agricultural University (Savary et al. 1990).

Structure of the Model

The system under study is a square meter of peanut crop infected by rust. The time step used is one climatological day. Processes with time coefficients smaller than one day are incorporated into daily input features. The model has two main units: crop growth and development, and rust epidemic, coupled together. The latter includes two subunits: rust lesion development, and rust multiplication. In the development of the model, due attention was given to leafspot, which affects crop growth and the rust epidemic.

The model used to simulate crop growth is SUCROS (Van Keulen et al. 1982). Four categories of organs are considered: roots, stems, leaves, and pods, represented by their respective dry weights. The parameters used were estimated from field data (e.g., partition coefficients), or collected from literature.

The infection cycle of peanut rust is simulated according to an early systems model by Zadoks (1971) with four categories of sites: vacant, latent, infectious, and removed lesions. Descriptions of lesion development incorporate cultivar resistance characteristics. Simulation of the canopy spore content involves temperature and cultivar effects on spore production, and a loss of spore due to rain leaching. Three phases are considered to simulate spore dispersal: liberation, deposition, and infection. Each have time coefficients smaller than one day and are incorporated into daily input features. Maturation and survival of deposited spores is also described.

Coupling

Coupling the two units of the model implies:

a) reconciling the dimensions used in each of them (dry matter and LAI units vs. sites and spore numbers)

b) describing the damage caused to the crop by rust and leafspot,

c) describing the interaction between host growth and rust epidemic

d) describing the effect of leaf spot on the host, and on the rust epidemic.

The coupling between the host and the parasite submodels is provided by two couplers (Zadoks and Rabbinge 1985): in the LAI to SITE direction: SITECO, the number of sites per LAI unit, and in the SITE to LAI direction: PSIZE, the leaf area occupied by one pustule.

Two rust damage components are considered: a reduction of photosynthetically active leaf area, and a flow of carbohydrates used for spore production, which is directly derived from the net photosynthetic rate before any partitioning to the growing organs. Three leaf spot damage components are considered: a reduction of photosynthetically active leaf area, defoliation, and compensation for defoliation.

Crop growth affects the rust epidemic in three ways: the trapping surface of the canopy varies with its LAI, canopy growth makes new sites available for infection, and defoliation reduces the amount of available and occupied sites.

Multiplication and radial growth of *Cercospora* lesions leads to destruction of occupied sites, which is represented by additional terms for the rates of rust lesion mortality in their various stages. This effect is superimposed on that of defoliation.

Model Performances

Evaluation of the model involves verification runs, and comparisons of model outputs with observed data (Teng 1985).

Variations of the daily multiplication factor (Zadoks 1971) and of the pustule spore content with varied weather conditions were found to correspond to the rules introduced in the model. Both variables are in balance, within a range of values which fits estimated values in the field. Various combinations for the values of the varietal coefficients produced a hierarchy of components of resistance which corresponds to observed results from a range of peanut cultivars, and agrees with previous simulation results using similar system designs for the pathogen unit (Zadoks 1971; Teng et al. 1977).

Simulated outputs were compared to actual data representing three separate epidemics, using the living leaf area index and rust severity as reference variables. The similarity between simulated and observed curves, with respect to the timing of the peaks, the day of epidemic upsurge, and the slope of the curves, is encouraging.

In view of its relative simplicity, the performance of this peanut rust simulation model may be considered to comply with the requirements which should be expected from a preliminary model. Several improvements, especially in the crop growth unit, may be considered to increase the explanatory value of the model, and allow its further development.

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Incorporation of Damage Mechanisms of Leaf Blast into the Crop Growth Model MACROS.

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Some well-documented growth models for rice have been recently developed (Penning de Vries et al. 1989; Alocilja 1988). In this study the MACROS-model was used to quantify yield reduction due to *Pyricularia oryzae* based on the pathogen's effect on plant physiological processes. This approach is characterized by the use of knowledge at the process level to explain phenomena at the systems level.

Pyricularia oryzae is the causal organism of rice blast. During the vegetative phase of the rice crop infection results in the formation of elliptically shaped lesions, mainly on the leaves. After flowering, infection of the neck or parts of the panicle occur, thereby directly effecting kernel yield. The present study was only on the effect of leaf blast on various basic processes was studied.

A pathogen may interfere with plant growth processes or existing biomass in various ways (Boote et al. 1983; Rabbinge and Bastiaans 1989). For *P. oryzae* on rice four potential damage mechanisms were identified. A reduction in assimilation rate of infected leaves is the first mechanism. Due to the formation of lesions the photosynthetically active part of the leaf is reduced. With some pathosystems this reduction in green leaf area fully explains the reduction in assimilation rate (van Roermund and Spitters 1990). However, in other pathosystems the effect on the pathogen is not limited to the lesions (Rabbinge et al. 1985).

A second damage mechanism is an enhanced respiration rate. This effect can be attributed to a combination of fungal respiration and an increased metabolic activity of the plant. A third damage mechanism is the use of photosynthetically produced assimilates for growth and reproduction of the pathogen. Finally, the longevity of infected leaves may be shortened as a result of the presence of the pathogen.

Quantification of all these effects would be too time consuming. Therefore a classification of the damage mechanisms on the basis of the expected contribution to yield reduction was made. First priority was given to the reduction of the photosynthetic capacity of infected leaves, since the pathogen is able to produce toxins and through this, its effect may exceed the boundaries of the lesion. To elucidate the relation between the fraction of visibly diseased leaf area (severity) and reduction of leaf photosynthesis, measurements in the greenhouse were done. These measurements demonstrated that the influence of the pathogen is not restricted to the visibly affected part of the leaf. In fact, it was shown that the reduction due to a single lesion is comparable to elimination of leaf area, 3 to 4 times larger than the lesion. If more lesions are present the ratio between real and visibly affected leaf area is reduced, comparable to the effect of overlapping lesions.

Introduction of this reduction into the crop growth model was the next step. With the MACROS model, daily crop assimilation is calculated by integrating momentaneous rates of photosynthesis of several leaf layers over canopy height and over the day. Momentaneous rates of photosynthesis are calculated from the amount of absorbed radiation by the leaf layers and the photosynthesis-light response curve of individual leaves. This procedure enables a straightforward introduction of the pathogen's effect on leaf photosynthesis. This effect can be introduced by including the experimentally determined relation between severity and the parameters that describe the photosynthesis-light response curve.

After introduction, comparison of models results with field experiments must clarify

whether growth and yield reduction is sufficiently explained by this damage mechanism. If this is the case, the model can be used to improve quantification of yield reduction caused by the pathogen under various circumstances. On the other hand, when growth and yield reduction is not simulated properly, introduction of another mechanism will be needed to increase correspondence between simulation and field experiments. Collection of data for validation thus continues.

Results of model calculations indicate that an epidemic in the vegetative phase causes a reduced formation of leaf and root dry weight. However, the effect on final kernel yield is negligible as long as the green area index around flowering exceeds a value of four. In situations with ample water and nutrients, such a value can only be reduced through very high severity levels. Further, the model shows that an epidemic which continues after flowering affects kernel yield directly since a reduced supply of assimilates in that phase reduces kernel filling.

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Can Pests and Crops Be Modeled with Standard Meteorological Data?

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How Weather Variables Relate to Each Other

The relationship between weather variables is apparent when an expansion of the energy balance is considered. For example, cloudiness reduces incoming solar radiation which in turn reduces energy available for warming and humidifying the air. In addition, clouds may be associated with rain and increased humidity on later days. During the day a dry surface will be heated and warm the air, but supply little water to the air. Wind can increase evaporation rates if water is available, but increased mixing also keeps near-surface humidity and temperature similar to humidity and temperature further above the surface.

It is useful to express humidity in terms which don't change much with other weather conditions. Relative humidity varies greatly as temperature changes during the day even without changes in the amount of water in the air. Consequently, vapor density, vapor pressure, or dew point temperature are preferable to relative humidity for many purposes.

Strategies for Filling Missing Data

There are no standard methods for filling in missing data. The following questions can guide selection of a strategy for filling data (Rosendahl, Schroeder, and Tagamori, personal communication; California Irrigation Management Information System):

- -Is data missing because of a meteorological extreme such as lightning?
- -How much data is missing, hours, days?
- -What type of measurement is missing, periodic, aperiodic?
- -Is the value needed for long term cumulation or averaging or does the individual value have significance?
- -Are there known air mass changes?
- -Is the value a minimum or maximum?
- -Is simultaneous data available from other sensors at this location?
- -Are there nearby sensors at this location?

For periodic values such as temperature, humidity, evaporation, and sometimes wind, with a diurnal cycle, the approach depends on the amount of missing data (in order of accuracy): 1) Estimate a smooth curve for the day; 2) correlate with a nearby station for the same day; 3) Use data from a near day for the station; 4) Correlate data from a near day for a nearby station; 5) Modify the average year values for this year; 6) Use values from an average year.

Nonperiodic data such as rainfall is best estimated from nearby stations using a correlation; however, thunderstorms, for example, can be non uniform.

Weather Station versus Canopy Height Measurements

Differences occur between weather station data, collected for example, at 2 m, and canopy measurements because of a number of causes: 1) local variability from topography, land use changes, wind breaks, etc. (State of Hawaii 1982); 2) rapid changes in conditions near the surface over height and time (Rosenberg et al. 1983); 3) Differences between plant and air temperatures due to transpiration, etc. (Oke 1987); 4) Great, small-scale spatial variability in within-canopy environmental conditions (Graser et al. 1987).

Calculation of Leaf Wetness

Condensation depends on the leaf energy balance, which in an expanded form is: $a(1+r)S + a_{IR}\delta[(T_{surr})^4 + (T_{sky})^4] - 2e_{IR}\delta(T_{leaf})^4 - 2K_{air}(T_{leaf}-T_{air})/[0.4(l/v)^{1/2}] - L2D_{wv}(q_{leaf} - q_{air})/[0.4(l/v)^{1/2}] = 0$

(see Nobel 1974 for variable names; Monteith 1973; Goudriaan 1977) for a thin horizontal, upper leaf on the basis on unit area for one side of the leaf assuming that the boundary layer thickness and rate of water supply is equal on both sides of the leaf. Cloudless nights, high humidity, low wind, and large leaves favor condensation by allowing the leaf temperature to reach the dew-point temperature of the air. The rate of formation and loss of condensation can be calculated by solving the energy balance for the water-vapor flux part of the latent-energy term.

a, r, a_{IR}, δ, e_{IR}, K_{air}, l, 0.4, L, and D_{wv} can be considered constants. S, T_{air}, q_{air}, and v can be estimated from hourly meteorological data. T_{surr}, T_{sky}, and T_{leaf}, (q_{leaf}) are usually unavailable or require much greater approximation.

Is Standard Meteorological Data Adequate for Pest Modeling?

The adequacy of standard meteorological data for pest modeling depends on the project goals, including the amount of detail necessary for the model, and prediction of the pest. How close do you need to approximate reality?

Regional meteorological data can be used for estimating average conditions for uniform regions such as water use and growing degree days by climatological methods.

Spatial distribution of conditions such as temperature and humidity near leaves in the crop microclimate, as opposed to in air spaces, can not be modeled in detail because crop models are missing processes of transport such as transport of heat and water vapor. Process models of the microclimate assume one-dimensionality or neglect non-gradient flow. Without spatial detail, whole habitats of certain pests will not be predicted. Process-level models may be eventually developed which are capable of modeling details of the crop microclimate conditions which can in turn be run with standard meteorological data.

The time interval of data collection is important when crops and pests are related to weather parameters in a nonlinear fashion. For example, due to a curvilinear suppression of mosquito activity with increasing wind speed, mosquito catches during nights with uniform winds are much less than catches during the nights with increasingly gusty winds with the same average wind speed. Consequently, average night time wind speed can not replace short-interval wind speed for predicting how mosquito catch relates to mosquito population.

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Linking A Model For Soybean Cyst Nematode with SOYGRO

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The subjects of this modeling effort are the soybean plant, *Glycine max*, as emulated by the SOYGRO model, and the soybean cyst nematode, *Heterodera glycines*. The plant and nematode can each be thought of as a collection of structures linked by processes. Examples of plant structures would include roots, stems, leaves, flowers, and pods. Processes which determine the amounts of each structure are photosynthesis, respiration, carbon partitioning, water and nutrient uptake, nitrogen fixation, translocation, flowering, etc. Nematode structures are the egg, juvenile stages, and the adult stage. The processes which govern these stages are hatch, penetration, establishment of a feeding site, development, and reproduction. Linkage of the plant and nematode models can be addressed by asking how the structures and processes of one organism have an impact on the structures and processes of the other organism. Modeling the dynamic interactions requires the use of mechanistic models of the plant and the nematode which have been constructed with appropriate hooks to facilitate connecting the models. SOYGRO, one of the IBSNAT models, has been documented elsewhere and will not be further discussed here.

The nematode model, SIMCYST, models the movement of individuals through functional stages of the life cycle. Functional stages were defined to maximize within stage similarity and between stage difference in terms of the interaction of each stage with the plant. Egg, infective juvenile, parasitic juvenile, and adult were chosen as the functional stages. The second-stage juveniles were divided between the infective and parasitic functional groups depending on whether or not they had established a feeding site and begun feeding. Second-stage juveniles which were feeding and the third- and fourth-stage juveniles were grouped together into the parasitic juvenile stage. The second-stage juveniles which had not yet penetrated the root and established a feeding site were classified as infective juveniles. The egg and adult stages matched the morphological stages. The functional stages were each further divided into substages to facilitate distributed development of the population. Each substage in the range of 70 to 130% of the mean duration for that stage was assigned a value for the probability of maturing to the next stage. The probability was calculated from an Erlang distribution based on the mean and standard deviation for the stage duration. Substages younger than 70% of the mean were considered too young to mature to the next stage. This method simulates the variability of developmental rates observed in natural populations. Penetration by the infective juveniles is not a developmental process. The youngest individuals have the highest probability of success which then drops off rapidly with age. An exponential function is a better descriptor of this process than the Erlang function. Survival is distributed over the substages by applying the "n^{th}" root of the whole stage survival to the exit of individuals from each substage where "n" is the number of substages completed after the mean stage duration. An individual which matures faster than the mean, incurs a lower mortality factor, whereas a slower developing individual has a higher mortality rate.

Linkage of SOYGRO and SIMCYST can be accomplished by quantifying the interactions of the structures and processes of each organism with the structures and processes of the other. The nematode must divert some of the available carbon for its own growth and reproduction. The position of the nematode in the priority list for carbon partitioning must be determined. Less carbon will be available for growth of any plant organ lower on the priority list than the

nematode. The amount of carbon demanded by the nematode will be a function of the total nematode population in the root and the population age structure. Nitrogen balance can be strongly affected by the nematode. Colonization of the roots by nitrogen-fixing bacteria can be suppressed up to 100% depending on the nematode population level and the particular plant-variety/cyst-nematode-race combination. The impact of the nematode on carbon and nitrogen balances alone can account for many of the commonly observed field symptoms such as chlorosis, stunting, and reduced stand. Plant health status is a strong indicator of a plant's ability to support a nematode population. Changes in the plant health status will have an impact on various parts of the nematode life cycle. A plant-produced hatching factor stimulates the eggs to hatch. The size of the healthy (not yet infected) root system determines how many of the newly-hatched infective juveniles will be able to penetrate and set up a feeding site. Resistant varieties allow the nematode to penetrate the root, but not establish a feeding site. The nematode's ability to develop and reproduce depends upon the amount of carbon available to it for growth.

Some of the information on plant/nematode interactions is currently available, but generally in a qualitative rather than quantitative form. There is still much research to be done in order to obtain the information needed to realistically link the soybean cyst nematode model to the soybean plant model.

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MODELING RICE-WEED INTERACTIONS

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Resource competition between crops and weeds is one of the major biological constraints to agricultural production. Although increasing quantities of herbicides have been applied in the recent past, weed problems have not been eliminated. Therefore, improved weed control strategies based on a thorough understanding of relevant interactions between crops and associated weeds is required. In this respect simulation models may provide fundamental information on growth and development of competing plants, and allow detailed insight into dynamic quantitative relationships between competitors growing in a natural environment.

Here, the competition for light and nitrogen between rice and associated weeds is presented as part of a rice ecosystems model. This model uses demographic theory and the metabolic pool approach (Jones et al. 1974; Gutierrez and Wang 1976; Gutierrez and Baumgärtner 1984a,b; Gutierrez et al. 1988) to describe carbon and nitrogen dynamics within and between population subunits on the same and different trophic levels. Three main processes drive the dynamic development of each population : a) Resource (solar radiation, carbohydrates, nitrogen) acquisition, b) allocation, and c) ageing and mortality (Fig. 1). Two processes link the different populations and account for population interactions: resource competition, and d) acquisition (Fig. 1).

a) Resource acquisition follows an analogous pattern on different trophic levels and may generally be considered as a predation process. A generalized form of the Frazer-Gilbert (1976) functional response model from predation theory is therefore used to quantify the flow of resources between different trophic levels. The acquisition rate is described as a function of resource availability on the next lower trophic level, the demand of the population, and the ability of the population to access the resources. Obviously, gains on one trophic level imply losses on the next lower level.

b) Resource allocation within a population is controlled by a priority scheme. Resources are normally used in decreasing order for respiration, reproduction, vegetative growth, and reserves.

c)Ageing and mortality of population subunits occurs on a physiological time horizon and is simulated with a time distributed delay model (Manetsch 1976; Vansickle 1977; Severini and Baumgärtner 1990) to account for the variance in mean longevity.

d) From a simplified point of view population interactions may be summarized as predation (see (a)) and competition processes. The latter are characterized by population attributes which determine the ability to access resources (Graf et al. 1990b).

Rice growth and development is modeled by applying the three basic processes of resource acquisition (a) allocation (b) ageing and mortality (c) (Graf et al. 1990a). Photosynthesis consequently can be described as a function of solar radiation (resource availability), potential growth and respiration rates of plant subunits (demand), and light interception (ability to access resource). According to the allocation scheme photoassimilates are used first for maintenance respiration and, with decreasing priority, for grain, culm, leaf, root growth and reserves. Carbohydrate supply/demand ratios scale down potential growth rates which, for their part, control the daily input into the delay routine.

Utilizing the same concept of resource acquisition, potential nitrogen uptake is a function of available soil nitrogen (resource availability), potential demand for nitrogen in newly grown plant tissue (demand), and root space explored (ability to access resource). N recycling from

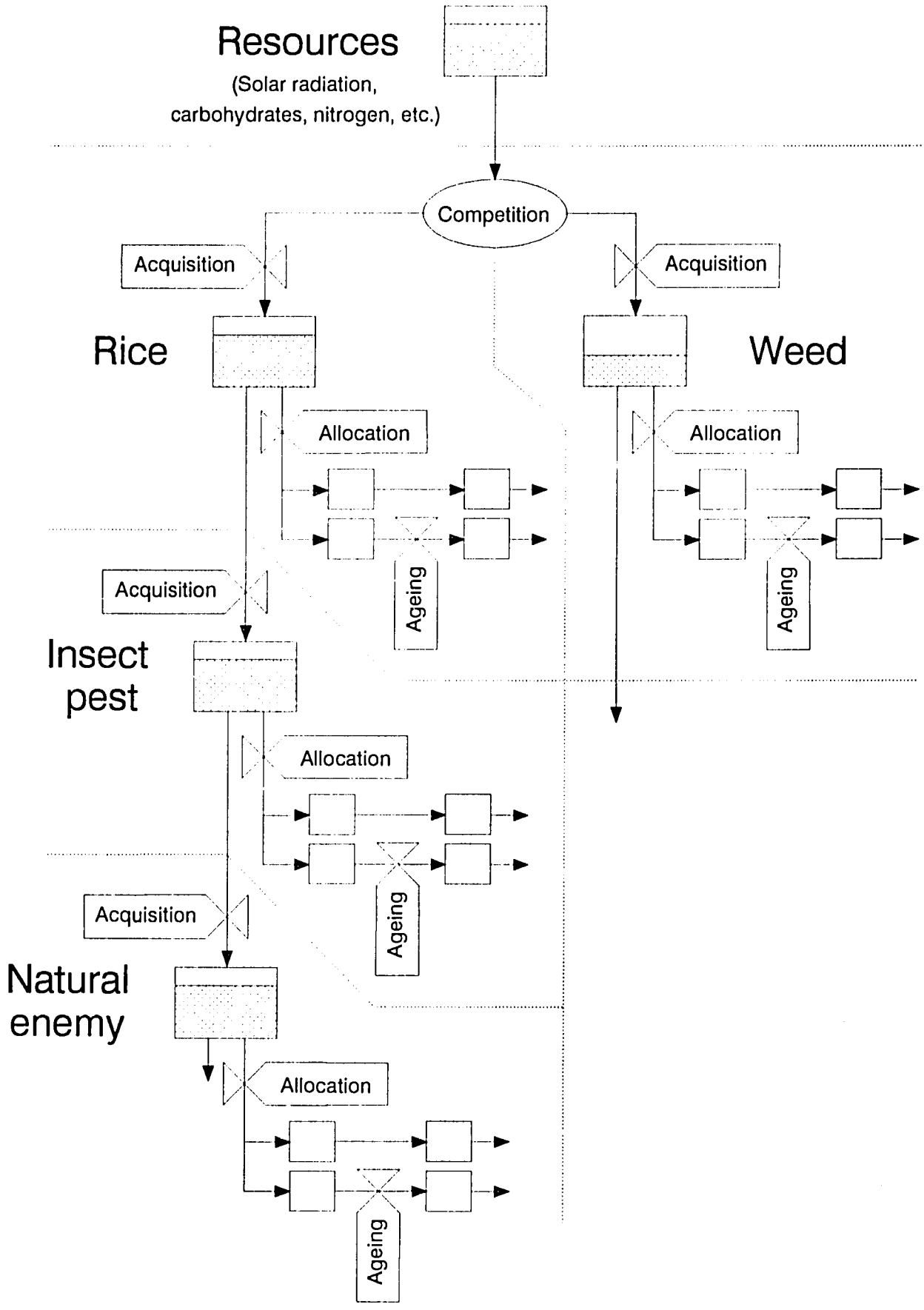

Fig. 1: Flow of resources within and between trophic levels

older plant tissue is taken into account when computing actual nitrogen uptake. The ratio of current N in the plant to the theoretical maximum is a measure of nitrogen stress which scales down the photosynthetic rates.

The submodel for weed growth uses the same notion of plant growth and is structured in a similar way as is the rice model, including carbon and nitrogen dynamics (Graf et al. 1990b). For reasons of simplicity the naturally occurring weed flora is divided into six weed groups which differ in development, phenology and morphology: Tall *Cyperaceae*, small *Cyperaceae*, *Gramineae*, other *Monocotyledoneae*, tall *Dicotyledoneae* and small *Dicotyledoneae*. Growth and development of each group is simulated separately.

In the model the different plant populations (rice and six weed groups) are interacting through light and nitrogen competition (d) (Graf et al. 1990b). The average plant height and spatial distribution of the leaf area, the key factors for light competition, determine the respective share of solar radiation available for each competitor (Spitters and Aerts 1983; Graf et al. 1990b). Root mass and explored root space, the main elements in nitrogen competition, are used to establish the partitioning pattern for available soil nitrogen among competing plants (Graf et al. 1990b).

Different data sets were used to validate the rice-weed competition model and its components. Field data on growth and development of MK 34 (a local rice variety from Madagascar), IR 58 and IR 64 (high yielding varieties from the Philippines) allowed the validation of the model with respect to carbon and nitrogen dynamics in rice without weed competition (Graf et al. 1990a,c). The model proved to have a sufficient validity range to satisfactorily simulate not only dry matter growth and development but also the nitrogen dynamics under various climatic conditions. It reacts correctly to increased planting densities and to different nitrogen fertilizations.

Experimental data collected in Madagascar were used to test the model predictions with respect to rice weed competition (Graf et al. 1990b). The model seems to capture the relevant interactions in the rice-weed association and describes the population dynamics of each competitor in a satisfactory manner. Under the field conditions recorded in Madagascar, light competition contributes 60% and nitrogen competition 40% to rice biomass losses. The effect of different weeding strategies on the development of rice and weeds are properly reproduced by the model.

Finally, the model allows for simulation of the effects of weed density, and timing of mechanical weed control on rice yield losses.

The encouraging results from the validation procedure demonstrate that the model produces reliable predictions. It allows a better insight into the dynamics of rice-weed interactions and by this means might contribute to improve future weed control strategies.

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Making Orchard Models Work: A Framework for Decision Support Incorporating Automatic Climate Sensing, Disease models, and Expert Systems

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Objectives of Project

To reduce pesticide residue levels in apples while maintaining fruit quality.

To reduce expenditures on pesticides in apple orchards.

To provide a strategic delivery system using horticultural and modeling expertise.

To provide a focal point for the exchange of information between growers, consultants, and scientists.

To provide a network of stations recording meteorologic and crop phenologic data.

Approach

This project brings together both existing and developing technologies. Its final output is an information system with five major components.

1. Environmental sensing and remote data logging.

2. Graphics-based software that lets growers keep better spray and phenological records.

3. An expert system which gives growers management recommendations rather than disease warnings. The system will take account of previous management by the grower in providing tailored recommendations.

4. Models of disease and spray cover which provide information both to the expert system and directly to the grower.

5. A data base storing orchard meteorology, management and phenology. The data base makes it easy to add further models to the system without burdening users with additional input requirements.

Models will initially be adapted or developed for the following diseases: Apple Black Spot (*Venturia inaequalis*), Fireblight (*Erwinia amylovora*) and Apple Powdery Mildew (*Prodosphaera leucotricha*), as well as for integrated control of European Red Mite (*Panonychus ulmi*). When combined with calendar-based recommendations for other pests and diseases, these will provide a complete set of spray recommendations to the grower.

This is a proposal to develop a holistic, information-based system for orchard management. By putting existing research to work the system will meet the emerging needs of growers. In addition the system will provide a framework for further testing and development of decision support tools.

In the proposed system subscribers will receive a suite of decision support tools. Their PC

will be linked to a central computer storing up-to-date weather and spray details. Scientists will have the option of having access to a grower's data (at the grower's discretion), and the ability to maintain and improve the system's component software. Data loggers each serve a small number of nearby growers. Weather forecasts placed on the central computer will be accessed automatically by the growers software. The network configuration gives the timeliness, and communications capabilities of the centralized computer, with the control and ease of use of the PC.

Growers will record spray applications in an orchard data base via a graphical representation of their orchard's blocks and rows. Models will use the microclimate and spray applications recorded in the data abase to establish the threat posed by individual diseases. An expert system will sort through the factors involved in a spray decision for a particular orchard on a particular day.

The orchard data base will serve as the foundation on which these applications are constructed. Information entered and stored by one application will be readily available to any other. The consistency of the graphical interface will make the applications easy to learn and use.

Future Developments

The system as planned can read information to and from a regional data base. This gives a mechanism for disseminating a wide range of information of interest to growers. With the involvement of the wider business community the following information could be offered:

- Hourly news from critical markets
- Exchange rates
- Stock holdings at spray merchants

The information collected on orchards would improve harvest date and yield forecasting. With growers' consent this information could be automatically collected and amalgamated on a daily or weekly basis.

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Algorithms for Assessing Risk

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Formal analysis of risk attitudes using Bernoulli's principle (Anderson et al. 1977) is not possible when the risk preferences of the targeted individual (his or her utility function) is not known. Although this type of analysis probably represents the best approach for determining whether or not a particular strategy would be preferred over another, it cannot be universally applied without utility functions. Furthermore, the very fact that it requires knowledge of the risk attitudes of the decision maker also means that it loses generality over less specific methods. These less specific methods are useful in the evaluation of different cropping strategies, and can eliminate those that would not be chosen by risk averse decision makers. With minor changes, these methods can also be used to compare different agroecosystems.

The approach presented here uses simulation models to convert information about weather variability into more directly useful information about the probability of a given return. If cropping strategies, such as the application of fungicides or use of cultivars with host plant resistance, are being analyzed, then numerous replicate runs of a crop production model can be made to obtain a probability density function (pdf) of the variable of interest (typically return). This is then repeated using the same weather information but changing the parameters of the model regulating the cropping system (cultivar, pesticide application, fertilizer, irrigation etc.). This results in different pdf's for the different cropping strategies. The replicate runs are produced using representative historical weather files or weather generated with a weather simulator program. The model thus can be conceived of as a "black box" that converts the variability in the weather into variability in return. This is the approach used by the Decision Support System for Agrotechnology Transfer (DSSAT V.2.1) (IBSNAT Project 1989) to explore different cropping systems, but has yet to be applied to evaluation of disease control strategies.

However, risk analysis is usually performed with return as the variable of interest, while disease information over time is the usual product of pathogen simulation models. Disease data is converted to yield information either through a coupled plant growth model or empirically derived disease-loss relationships. Any variable costs involved in the different production strategies (application of pesticides, fertilizers, improved seed, etc.) must also be included in the calculation of a strategy's return to provide an economically realistic analysis. Limited analyses have been conducted with pathogen only models using only disease data. In these cases, it is assumed that producers would attempt to minimize area under the disease progress curve (AUDPC) or the final disease level, but these are perhaps unrealistic assumptions.

The pdf's for different strategies can then be compared using a number of techniques. In the simplest sort of analysis, the mean value of return for a given strategy is calculated. This is called the expected monetary value (EMV), and can identify those strategies that, on the average, would give the highest return. EMV alone does not take the variability of return into account, however, and the variance of the EMV can also be calculated from the pdf. For one strategy to be preferred over another, it must have a larger EMV, but a smaller variance.

A related technique is to use stochastic dominance (Hadar and Russell 1969; Meyer 1977) to compare two different strategies. The cumulative probability density function (cdf) of each strategy is calculated by taking the integral of the pdf. These cdf's are compared either numerically or graphically, with the x axis net return, and the y axis cumulative probability. If

one curve lies entirely to the right of another, it is said to dominate it (be preferred) by first degree stochastic dominance (FSD). If the cdf curves intersect, neither strategy dominates in FSD. Figure 1 is a comparison of two strategies (labeled Policy 1 and Policy 2) with FSD. Since the lines intersect, neither strategy dominates in FSD.

This procedure can then be repeated for second degree stochastic dominance. The integral of the cdf can be calculated, yielding a second set of curves that can be compared in a similar manner, with the x axis return, and the y axis the integral of the cdf. If one curve lies entirely to the right of another curve, it is said to dominate in second degree stochastic dominance (SSD). In the comparison in Figure 2, Policy 2 dominates Policy 1 by SSD. Strategies that dominate in SSD are said to be preferred by decision makers that are averse to risk. Third and even fourth degree stochastic dominance comparisons can be made, but their interpretation is more difficult.

This technique can also be extended to compare the same cropping system in different locations. In this case, instead of varying the parameters that affect the cropping system and keeping the weather files or weather generator constant, the parameters regulating crop production are held constant and the pdf's are generated for weather files or generators representing different locations.

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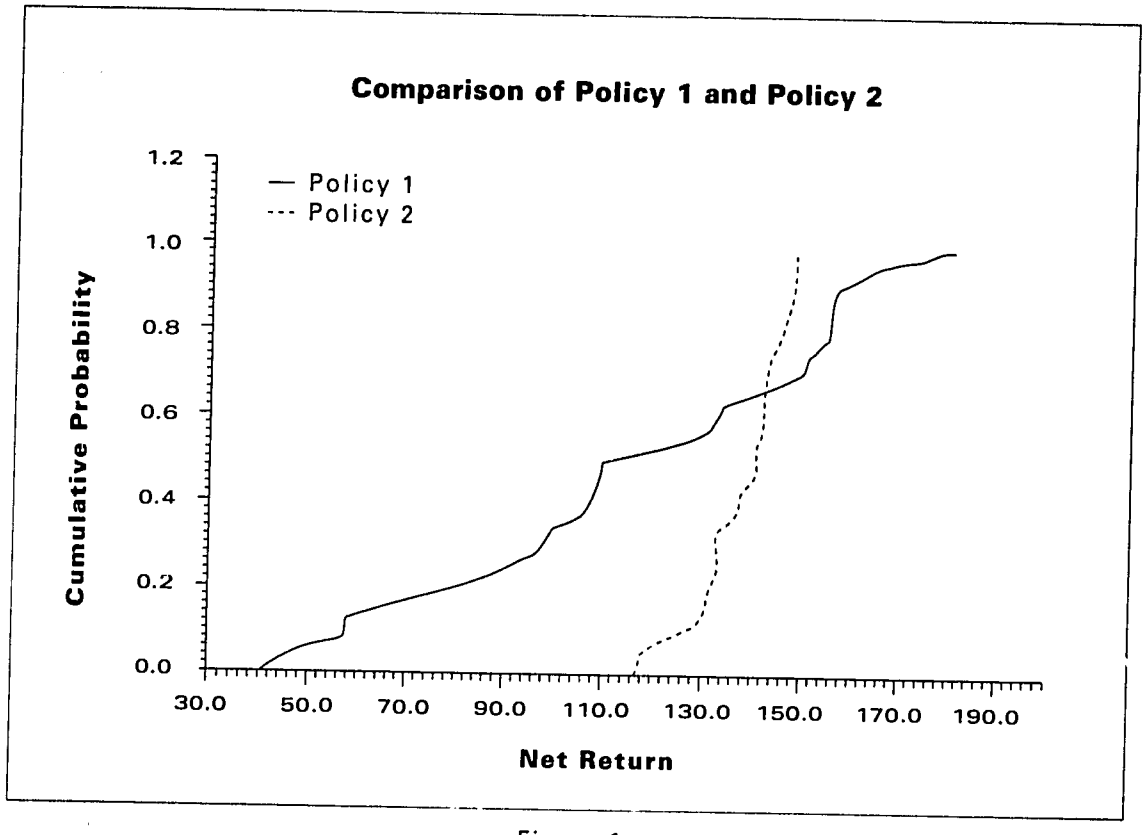

Figure 1

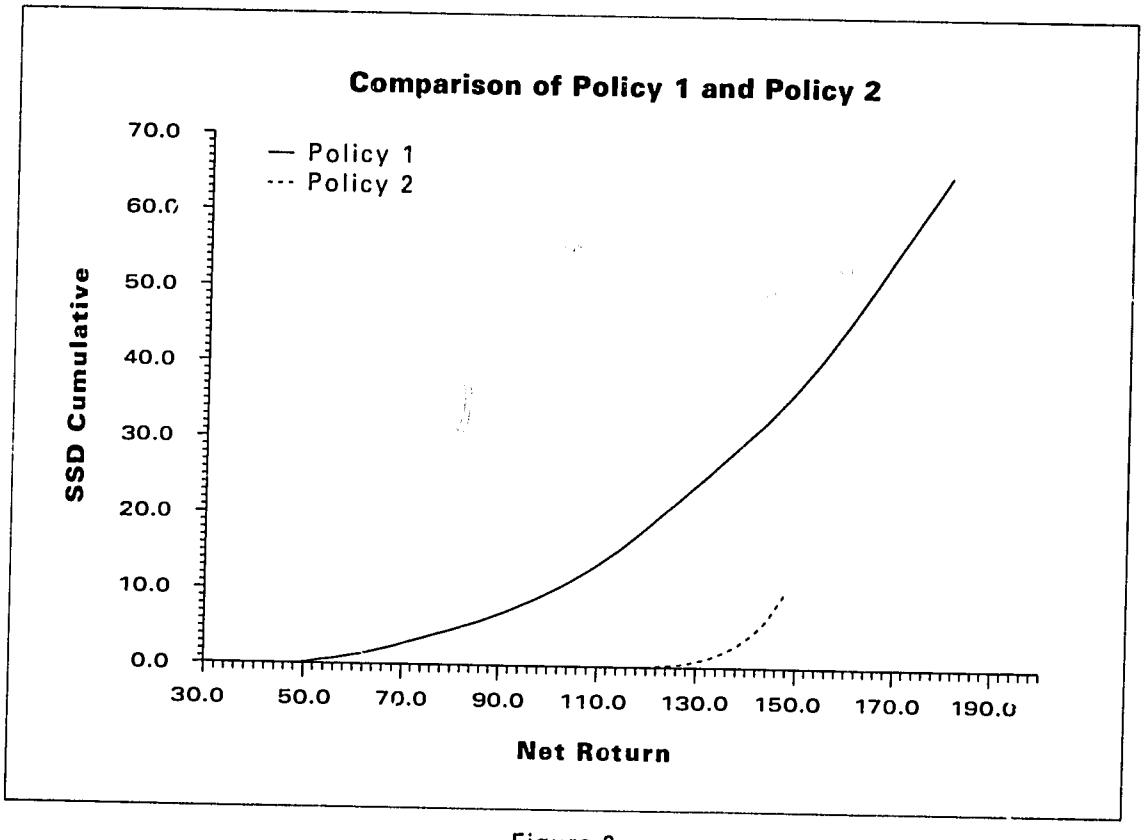

Figure 2

The use of Modeling and Nonmodeling Approaches in Field Testing Genetically Engineered Microorganisms

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The basic purpose of using modeling approaches in field testing genetically engineered organisms is the efficient use of resources in designing safe and valid experiments. At present, limited data are available to model potential effects of genetic manipulations in regard to their intended function, genetic stability, rate of exchange of genetic material, persistence, etc. I, therefore, consider that the primary objective of modeling approaches at the moment are to develop and test containment strategies for field testing genetically released organisms. They could provide the framework for the development of models dealing with the genetic fate of the microorganisms (MO), such as:

1) The loss of the genetic trait over time
2) Persistence of the genetic trait over time
3) Rate of migration of the trait into related, but unmodified MO.
4) Rate of migration of the genetic trait into unrelated MO.
5) Pleiotropic effects, cascade effects.

At present, modeling approaches could be useful in the following areas:

1) Assess the fate and behavior of released microorganisms in the environment. Models in this category involve the simulation of spread, survival, multiplication, etc. of the organism.

2) Assess the suitability of potential release sites or assist in the choice of potential sites. Models in this category could be useful in determining the suitability of sites in regard to runoff, groundwater intrusion of the MO, erosion, etc. as possible vectors the MO could utilize to escape the confinement.

3) Assist in experiment designs. Models in this category could be useful in determining potential sites where the MO can be found in the experimental area. This information could form the basis for efficient sampling strategies.

4) Develop standard testing protocols and/or guidelines specific for MO groups. Models in this category could be used to simulate various containment techniques and determine the most efficient approaches dependent on the characteristics of the MO.

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5) Provide a scientific basis for the regulatory agencies. Models in this category could be used by regulatory agencies to evaluate the effectiveness of methodologies proposed for planned releases.

The following is an incomplete survey of available models that could be used in the above mentioned categories.

Transport Media	General Description	Models/Reference
Air	Estimate dispersion of small particle aerosols from point sources-Gaussian plume is basic model- includes die off, impact of aerosolization on microbial surviva	ATM-TOX/Raridon et al. 1988 ISC/Bowers et al. 1979
Surface Runoff	Estimate microbes in suspension transported in runoff and attached to soil particles (erosion)-based on distance to surface water, rainfall, and topographical	Usle/Wischmeir and Smith 1965. Creams/Moore et al. 1988 AGNPS/Young et al. 1982. WLFNPS/Haith and Tubbs 1981.
Soil	Estimate the location and concentration of MO-Model the emigration rate-includes interception, sedimentation, diffusion, attachment/detachment absorption/desorption, pore clogging/declogging	Microbe Screen/Reichenbach et al. 1987 O'Melia 1985 Corapcioglu and Haridas 1984, 1985
Groundwater	Estimate MO fate using one-,two-, or three dimensional models	Random Walk Code Prickett et al., 1981 MOC/Konikow and Bredlehoeft, 1983

Parameter	General Description	Models/Reference
Survival-Air and Water	Estimate MO survival in fate models-functions include die-off, unlimited and exponential growth, steady state and substrate limited growth	Crane and Moore 1985 Reichenbach et al. 1987 Paris et al. 1982
		Competition
		Involves reproduction selection coefficient
		MacKenzie 1984 De Wit 1960 Lottka-Volterra equation

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